

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re application of: ) Examiner: Kemmerer, Elizabeth  
                          ) )  
Audrey GODDARD, *et al.* ) Art Unit: 1646  
                          ) )  
Application Serial No. 09/902,713 ) Confirmation No: 1320  
                          ) )  
Filed: July 10, 2001         ) Attorney's Docket No. GNE-1618 P2C34  
                          ) )  
For: **ANTIBODIES TO PRO269** ) **Customer No. 77845**  
**POLYPEPTIDES**

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Filed Via EFS January 2, 2009

**ON APPEAL TO THE BOARD OF PATENT APPEALS AND**  
**INTERFERENCES APPELLANTS' REPLY BRIEF**

**MAIL STOP APPEAL BRIEF - PATENTS**  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, Virginia 22313-1450

Dear Sir:

On November 7, 2007 and November 30, 2007, the Examiner made a Final rejections to pending Claims 39-43. A Notice of Appeal was filed on February 20, 2008 and an Appellants' Appeal Brief was subsequently filed May 20, 2008. In response to Notice of Non-Compliant Appeal Brief, a Supplemental Brief was filed on July 2, 2008 providing a corrected summary of the claimed subject matter.

An Examiner's Answer was mailed on November 4, 2008. The following constitutes Appellants' Reply Brief in response to the Examiner's Answer. This Reply Brief is accompanied by a Request for Oral Hearing.

## ARGUMENTS

### **1. Claim Rejections Under 35 U.S.C. §101 and §112, First Paragraph**

Concerning the rejection of Claims 39-43 under 35 U.S.C. §101 as allegedly lacking a specific, substantial and credible asserted utility or a well established utility, in his Answer, the Examiner cites the following arguments:

(1) The instant rejections are primarily based on whether or not genomic DNA levels (as measured by the gene amplification assay) correlate with either mRNA levels or polypeptide levels. The Examiner asserts that the Goddard declaration is insufficient to overcome the rejection because “while [it] speaks to the utility and enablement of genes, it does not speak to whether or not the encoded polypeptides are also found at increased levels in cancerous tissues.” (Examiner’s Answer, page 15) The Examiner addresses the pooled blood controls used in the gene amplification assay and asserts that the controls were not matched, non-tumor lung samples, but rather pooled DNA samples from blood of healthy subjects. (page 15 of Examiner’s Answer). The Examiner further asserts that “PRO269 was reported as being amplified in less than half of the lung tumor samples tested.” (page 5 of Examiner’s Answer).

(2) The Examiner alleges that the Ashkenazi declaration actually supports the Examiner’s position in that it “contradicts the assertion of utility in the specification, wherein the specification indicates that gene amplification is associated with protein over-expression but Dr. Ashkenazi indicates that this is not always the case.” (page 28 of the Examiner’s Answer).

(3) The Examiner asserts that references such as Pennica *et al.*, Konopka *et al.*, Hanna *et al.*, Sen *et al.*, Hittelman *et al.*, Godbout *et al.*, and Li *et al.* constitute strong opposing evidence for the claimed polypeptides having utility and enablement, based on the presumption that the claimed polypeptides are also overexpressed following gene amplification (page 15 of the Examiner’s Answer). Referring to the references by Sen and Hittelman, the Examiner alleges that, in general, non-cancerous epithelial tissues are frequently aneuploid, and thus an increase in genomic DNA is not diagnostic of cancer (page 6 of the Examiner’s Answer). Based on the Pennica *et al.* and Konopka *et al.* references, the Examiner asserts that these references constitute evidence that it cannot be assumed that amplified genomic DNA results in overexpressed gene product (Examiner’s answer, pages 7-8). The Examiner also quotes Godbout

as stating: “*It is generally accepted that co-amplified genes are not over-expressed unless they provide a selective growth advantage to a cell...*” and thereby inquires whether Appellant can show evidence for PRO269 providing a selective growth advantage to a cell (pages 8-9 of Examiner’s Answer).

(4) Regarding the supportive references Orntoft *et al.*, Hyman *et al.* and Pollack *et al.*, made of record by the Appellants, and which clearly address gene amplification, the Examiner considers them flawed. The reasons cited were: Orntoft *et al.* only compared levels of about 40 well-resolved and focused on abundant proteins; Hyman *et al.* found 44% of highly amplified genes showed overexpression at the mRNA level, and 10.5% of highly overexpressed genes were amplified and even at this level of high amplification and high overexpression, the two did not correlate; Pollack *et al.* is also limited to highly amplified genes and used a different method to evaluate their results (pages 19-20 of Examiner’s Answer).

Appellants strongly disagree with each of the Examiner’s arguments on a number of grounds. The Examiner’s arguments will be addressed in the order they are listed above.

#### **Reply to the Examiner’s arguments**

(I) The Goddard Declaration was presented to show what ΔCt values were considered significant in the TaqMan™ assay. The ΔCt values for the DNA that encodes for PRO269 showed **2.0-3.5 fold amplification in eight** different lung tumors or cell lines, which would be considered significant according to the Goddard Declaration. While this declaration addresses DNA values, it has been presented in this polypeptide case in conjunction with several other supportive references like Orntoft *et al.*, Hyman *et al.*, Pollack *et al.*, Bea *et al.*, Godbout *et al.*, etc. As explained previously, Orntoft *et al.*, Hyman *et al.*, and Pollack *et al.* were presented to show that in general, gene amplification increases mRNA expression. In addition, Appellants presented two Polakis Declarations (Polakis I and II) to show that, in general, mRNA levels correlate well with protein levels, and the Examiner seems to agree with this point especially in view of the recent Board Decision (Decision on Appeal No. 2006-1469) addressing microarray cases. Presentation of the Goddard Declaration is indeed relevant in this polypeptide case, because it forms a critical piece of evidence in this case. When placed together with the entire evidence presented for PRO269, one would logically come to the conclusion that, it is more

likely than not, that increased DNA levels generally correlate well with increased mRNA levels (based on, for example, the teachings of supportive references like Orntoft et al., Hyman et al., Pollack et al., Bea et al., Godbout et al., etc.), and further, increased mRNA levels generally correlate well with increased protein levels (the two Polakis Declarations and the recent Board decision). In summary, just as in the microarray cases, Appellants have presented multiple pieces of evidence, such as the Goddard Declaration, the Ashkenazi Declaration, two Polakis Declarations, several references addressing the relationship between DNA and mRNA/ protein levels, etc., each of which is critical evidence that supports Appellants' position that PRO269 polypeptides and the antibodies that bind them have utility based on the gene amplification results. Therefore, Appellants believe that a sound case has been presented for utility of PRO269 as a diagnostic marker, based on the gene amplification data of its corresponding gene in the specification.

Further, the Examiner is required to view the statements in the declaration with the total evidence presented in this case. The case law has clearly established that in considering affidavit evidence, the Examiner must consider all of the evidence of record anew (*In re Rinehart*, 531 F.2d 1084, 189 USPQ 143 (C.c.P.A. 1976); *In re Piasecki*, 745F.2d. 1015,226 USPQ 881 (Fed. Cir. 1985)). "After evidence or argument is submitted by the applicant in response, patentability is determined on the totality of the record, by a preponderance of the evidence with due consideration to persuasiveness of argument."( *In re Alton*, 37 USPQ2d 1578, 1584 (Fed. Cir 1996) (quoting *In re Oetiker*, 977 F.2d 1443, 1445,24 USPQ2d 1443, 1444 (Fed. Cir. 1992)). Furthermore, the Federal Court of Appeals held in *In re Alton*, "We are aware of no reason why opinion evidence relating to a fact issue should not be considered by an Examiner (*In re Alton, supra*). Appellants also respectfully draw the Examiner's attention to the Utility Examination Guidelines (Part II B, 66 Fed. Reg. 1098 (2001)) which state, "Office personnel must accept an opinion from a qualified expert that is based upon relevant facts whose accuracy is not being questioned; it is improper to disregard the opinion solely because of a disagreement over the significance or meaning of the facts offered." Appellants submit that the Patent Office has failed to provide substantial evidence for disregarding the Goddard Declaration.

Further regarding the Examiner's assertion that less than half of the lung cancer samples tested positive for PRO269 gene amplification, Appellants respectfully point out that they have

shown significant DNA amplification in three different primary lung tumor samples. The fact that not all lung tumors tested positive in this study does not make the gene amplification data less significant. As any skilled artisan in the field of oncology would easily appreciate, not all tumor markers are generally associated with every tumor, or even with most tumors. For example, the article by Hanna and Mornin (submitted with the Response filed May 21, 2004), discloses that the known breast cancer marker HER-2/neu is "amplified and/or overexpressed in 10%-30% of invasive breast cancers and in 40%-60% of intraductal breast carcinoma" (page 1, col. 1).

Appellants submit that the amplification of the PRO269 nucleic acids in even one lung tumor provides specific and substantial utility for the nucleic acid as a diagnostic marker of the type of lung tumor in which it was amplified. Appellants further note that the tumors listed in Table 9 are not similar tumors from different patients, but various types/classes of lung and/or colon tumors at different stages. Accordingly, a positive result from one tumor, where the nucleic acid was amplified, but not from other tumors, indicates that the nucleic acid can be used as a marker for diagnosing the presence of that kind of tumor in which it was amplified.

Amplification of the nucleic acid would be indicative of that specific class of lung tumor, whereas absence of amplification would be non-conclusive. The skilled artisan would certainly know that such tumor markers are useful for better classification of tumors. Therefore, whether the PRO269 gene is amplified in eight lung tumors or in all lung tumors is not relevant to its identification as a tumor marker, or its patentable utility. Rather, the fact that the amplification data for PRO2691 is considered significant strongly supports its usefulness as a tumor marker. If the goal is to diagnose lung cancer, then contrary to the Examiner's assertion, a positive result does indicate the presence of cancer, while a negative result is not conclusive, and requires follow up testing.

Regarding the rejection of pooled controls (addressed in the Goddard Declaration), Appellants respectfully point out that Pennica *et al.*, cited by the Examiner, teaches the exact same "pooled normal blood controls" as that used in the instant gene amplification assay (for instance, see page 14718, column 1 and Figure 5 of Pennica *et al.*). Further, the references Bieche *et al.* and Pitti *et al.*, submitted as Exhibits F and G with the Goddard Declaration, also used "pooled normal blood controls" as control. For instance, in Pitti *et al.* the authors used the

same quantitative TaqMan PCR assay and pooled normal blood controls described in the instant specification, to study gene amplification in lung and colon cancer of DcR3, a decoy receptor for Fas ligand. Pitti *et al.* analyzed DNA copy number "in genomic DNA from 35 primary lung and colon tumors, relative to pooled genomic DNA from peripheral blood leukocytes (PBL) of 10 healthy donors." (Page 701, col. 1). The authors also analyzed mRNA expression of DcR3 in primary tumor tissue sections and found tumor-specific expression, confirming the finding of frequent amplification in tumors, and confirming that the pooled blood sample was a valid negative control for the gene amplification experiments. In Bieche *et al.*, the authors used the quantitative TaqMan PCR assay to study gene amplification of myc, ccdn1 and erbB2 in breast tumors. As their negative control, Bieche *et al.* used normal leukocyte DNA derived from a small subset of the breast cancer patients (page 663). The authors note that "[t]he results of this study are consistent with those reported in the literature" (page 664, col. 2). Thus, contrary to the Examiner's allegations, Pennica *et al.*, Pitti *et al.* and Bieche *et al.* in fact, confirm the validity of use of the "pooled blood control" as a negative control, and indicate that this control was widely utilized in the art at the time of filing of the instant application. Appellants further submit that the Examiner's position is scientifically incorrect because the instant application relies on **genomic DNA** amplification for utility and not eDNA expression. Different types of cells from the same organism should have the same set of genomic DNA. Thus, it does not matter what kind of cells you use for the control as long as the control cells have the entire genome. Accordingly, a "tissue-matched" control is not necessary in the gene amplification assay.

(2) The Examiner alleges that the Ashkenazi Declaration actually supports the Examiner's position in that it provides further evidence that gene amplification does not always correlate with increased mRNA/polypeptide levels. First, "always" is not required by the utility standard. Second, this position of the Examiner is based on a complete misinterpretation of the Ashkenazi Declaration, its teachings and the arguments presented by the Appellants regarding this Declaration. Appellants fail to see how the Ashkenazi Declaration could support the Examiner's arguments when Appellants clearly stated that, even if there were no correlation between gene amplification and increased mRNA/protein expression, (**which Appellants expressly do not concede to**), a polypeptide encoded by a gene that is amplified in cancer would

still have a specific, substantial, and credible utility. Appellants submit that, based on the teachings of the Ashkenazi Declaration and the Hanna and Mornin reference (both previously made of record), one of skill in the art would have known that simultaneous testing of gene amplification and gene product over-expression enables more accurate tumor classification, even if the gene-product, the protein, were not to be over-expressed. This leads to better determination of a suitable therapy for the tumor, as demonstrated by a real-world example of the breast cancer marker HER-2/neu. Again, the presentation of this explanation in support of utility is not to be interpreted as a submission of a lack of correlation between DNA and/or mRNA/protein levels.

(3) Appellants have already discussed the references Pennica *et al.*, Konopka *et al.*, Sen *et al.*, Hittelman *et al.*, Godbout *et al.*, and Li *et al.* in great detail throughout prosecution and in their Appeal Brief filed May 20, 2008; these discussions and arguments are hereby incorporated by reference.

Briefly, the teachings of Pennica *et al.* are specific to *WISP* genes, a specific class of closely related molecules. Pennica *et al.* showed that there was good correlation between DNA and mRNA expression levels for the *WISP-1* gene but not for *WISP-2* and *WISP-3* genes. The fact that, for two out of three specific molecules there seems to be no correlation between gene amplification and/or mRNA/protein expression, does not establish that it is more likely than not, in general, that such correlation does not exist. As discussed throughout prosecution, the standard is not absolute certainty. Pennica *et al.* has no teaching whatsoever about the correlation of gene amplification and protein expression for genes in general. Indeed, the working hypothesis among those skilled in the art is that, if a gene is amplified in cancer, the encoded protein is likely to be expressed at an elevated level. In fact, as noted even in Pennica *et al.*, “[a]n analysis of *WISP-1* gene amplification and expression in human colon tumors *showed a correlation between DNA amplification and over-expression . . .*” (Pennica *et al.*, page 14722, left column, first full paragraph, emphasis added). Accordingly, Appellants respectfully submit that Pennica *et al.* teaches nothing conclusive regarding the absence of correlation between gene amplification and over-expression of mRNA or polypeptides in most genes, in general. Therefore, the teachings of Pennica *et al.* are not directed towards genes in general but to a single gene or genes.

within a single family and thus, their teachings cannot support a general conclusion regarding a correlation between gene amplification and mRNA or protein levels.

Regarding Konopka *et al.*, Appellants submit that the Examiner has completely misinterpreted the teachings in the cited reference. Contrary to the Examiner's assertions, Konopka *et al.* does not support the position that DNA amplification is not correlated with mRNA overexpression. Konopka *et al.* show only that, of the cell lines known to have increased abl protein expression, only one had amplification of the abl gene (page 4051, col. 1). This result proves only that increased mRNA and protein expression levels can result from causes other than gene amplification. Konopka *et al.* do not demonstrate that when gene amplification does occur, it does not result in increased mRNA and protein expression levels, particularly given that the cell line with amplification of the abl gene did show increased abl mRNA and protein expression levels. Furthermore, Konopka *et al.* supports Appellants' position that mRNA levels correlate with protein levels. Konopka *et al.* state that "the 8-kb mRNA that encodes P210<sup>c-abl</sup> was detected at a 10-fold higher level in SK-CML7bt-333 (Fig. 3A, +) than in SK-CML16Bt-1 (B, +), which **correlated** with the relative level of P210<sup>c-abl</sup> detected in each cell line. Analysis of additional cell lines demonstrated that the level of 8-kb mRNA **directly correlated** with the level of P210<sup>c-abl</sup> (Table 1)" (page 4050, col. 2, emphasis added).

The Examiner has further asserted that "Hanna et al. supports the rejection, in that Hanna et al. show that gene amplification does not reliably correlate with protein over-expression, and thus the level of polypeptide expression must be tested empirically." (Page 24 of the Examiner's answer). Appellants respectfully reiterate that the Examiner appears to have misread Hanna *et al.* Hanna *et al.* clearly state that gene amplification (as measured by FISH) and polypeptide expression (as measured by immunohistochemistry, IHC) are well correlated ("in general, FISH and IHC results correlate well" (Hanna *et al.* p. 1, col. 2)). It is only a subset of tumors which show discordant results. Thus Hanna *et al.* support Appellants' position that it is more likely than not that gene amplification correlates with increased polypeptide expression.

In contrast, in the majority of amplified genes, the teachings in the art, as exemplified by Orntoft *et al.*, Hyman *et al.*, Pollack *et al.*, overwhelmingly show that gene amplification influences gene expression at the mRNA and protein levels. Appellants submit that when the proper legal standard is applied, one of skill in the art should reach the conclusion, based on the

amplification data for the PRO269 gene, that the PRO269 polypeptide is concomitantly overexpressed, and that the present application discloses at least one patentable utility for the claimed antibodies to the PRO269 polypeptide. Accordingly, one of ordinary skill in the art would also understand how to make and use the recited antibodies for the diagnosis of lung cancer without any undue experimentation.

The Examiner contends that the Li article constitutes strong opposing evidence for the presumption that the claimed polypeptides are also overexpressed following gene amplification. Appellants respectfully disagree. The Li article was discussed extensively in the Appeal Brief filed May 20, 2008; these discussions and arguments are hereby incorporated by reference. In the article, genes were considered to be amplified if they had a copy number ratio of at least 1.40. In the instant case for PRO269, as discussed in the Goddard Declaration (of record), an appropriate threshold for considering gene amplification to be significant is a copy number of at least 2.0 (which is a higher threshold than Li's 1.40). The PRO269 gene showed significant amplification of **2.0- to 3.5-fold** in **eight** different lung tumors or cell lines, and thus fully meets the Goddard standard as well as the Li standard. Appellants further note, and it is not surprising that, in the Li *et al.* reference, by using a lower threshold of 1.4 for considering gene amplification, a higher number of genes not showing corresponding increases in mRNA expression were found. Nevertheless, the results of Li *et al.* do not conclusively disprove that a gene with a substantially higher level of gene amplification, such as PRO269, would be expected to show a corresponding increase in transcript expression. Therefore Li does not constitute opposing evidence.

In response to Appellants' argument that the discordance may reflect methodologic differences, the Examiner asserts that "Li *et al.* did not limit their studies to genes that were amplified at less than 2-fold." In support of this assertion, the Examiner cites the first paragraph of the Supplemental Material. (Pages 18-19 of the Examiner's Answer). Appellants respectfully point out that the Examiner has misinterpreted the Li *et al.* methodology disclosed in the supplemental material. The evidence cited by the Examiner pertains to the inclusion criteria of the probes used for defining amplicons. In the second paragraph entitled "Relationship between genomic copy number and gene transcript level", the authors state that "[f]or each gene, the CGH data were represented by a vector that was labeled '1' for genomic overrepresentation (including amplification) ratio greater than 1.40 and '0' for no genomic overrepresentation."

Nevertheless, the Examiner acknowledges that the alleged 2-fold amplification criteria would only apply to some of the samples examined by Li *et al.* The Examiner has not established that a correlation does not exist in samples based solely on this threshold.

Based on Godbout et al., the Examiner asserts “that the protein encoded by the PRO269 gene would confer any selective advantage on a cell expressing it” in the Examiner’s answer; in other words, the Examiner requests Appellants to show the mechanism by which the claimed protein acts within the cell. However, Appellants respectfully remind the Board that demonstration of the mechanism is not a requirement for attaining that utility. Appellants believe that such a requirement is a heightened utility standard imposed by the Examiner. In fact, as stated by the Federal Circuit, “it is not a requirement of patentability that an inventor correctly set forth, or even know, how or why the invention works.” *In re Cortwright*, 165 F.2d 1353, 1359 (Fed. Cir. 1999). The Federal Circuit has also stated that “[a]n invention need not be the best or only way to accomplish a certain result, and it need only be useful to some extent and in certain applications: “[T]he fact that an invention has only limited utility and is not operable in certain applications is not grounds for finding lack of utility.” *Envirotech Corp. v. Al George, Inc.* 730 F.2d 753,762, 221 USPQ 473,480 (Fed. Cir. 1984). ” Hence this rejection is improper.

Regarding the art exemplified by Sen *et al.* and Hittelman *et al.*, Appellants maintain their position that these references still support their case for the reasons outlined in their Appeal Brief filed May 20, 2008, which is hereby incorporated by reference. Briefly Appellants maintain that, even if the amplification of the PRO269 gene were due to chromosomal aneuploidy (which Appellants expressly do not concede to), since there is utility for an aneuploid gene at least as a marker for cancer or precancerous cells or damaged tissue, one skilled in the art would find it entirely reasonable that PRO269 is useful in the early detection of lung cancer. Regarding the data allegedly not being corrected for aneuploidy, Appellants reiterate that it is known in the art that detection of gene amplification can be used for cancer diagnosis regardless of whether the increase in gene copy number results from intrachromosomal changes or from chromosomal aneuploidy. As explained by Dr. Ashkenazi in his Declaration (submitted with Appellants’ Response filed October 16, 2003).

An increase in gene copy number can result not only from intrachromosomal changes but also from chromosomal aneuploidy. It is important to understand that detection of gene

amplification can be used for cancer diagnosis even if the determination includes measurement of chromosomal aneuploidy. Indeed, as long as a significant difference relative to normal tissue is detected, it is irrelevant if the signal originates from an increase in the number of gene copies per chromosome and/or an abnormal number of chromosomes.

Hence, Appellants submit that gene amplification of a gene, whether by aneuploidy or any other mechanism, is useful as a diagnostic marker.

(4) The Orntoft *et al.*, Hyman *et al.*, and Pollack *et al.* references were presented during prosecution to show that, in general, gene amplification increases mRNA expression. As Appellants have acknowledged, the correlation between changes in mRNA level and protein level is not exact, and there are exceptions. However, Appellants have submitted during prosecution over 100 references in addition to the declarations and references already of record which support Appellants' asserted utility, either directly or indirectly. This included references that studied single genes or gene families, multiple or large families of genes, and included studies that a wide variety of techniques, including gene amplification and microarray. Regardless of the techniques employed, by and large, increased gene levels generally correlated well with increased mRNA and /or protein levels, even if accurate predictions of proteins could not be made. As discussed throughout prosecution, the law does not require the existence of a "necessary" correlation between DNA/mRNA and protein levels, or that protein levels be "accurately predicted." In fact, authors in several of the cited references (cited both, by the Examiner, and by Appellants) themselves acknowledge that there is a general correlation between protein expression and transcript levels and DNA levels, which meets the "more likely than not standard." Therefore Appellants have explored this issue thoroughly throughout prosecution in the vast number of references presented in this case and the evidence should be viewed as a whole.

Regarding the Examiner's contention that references Orntoft *et al.*, Hyman *et al.*, Pollack *et al.* are flawed because, allegedly, their studies were directed to highly amplified genes or abundant proteins, Appellants have submitted that PRO269 is significantly amplified (according to the Goddard Declaration) throughout prosecution. Appellants believe that this significantly amplified DNA would more likely than not result in a higher expression of PRO269 protein,

according to the teachings of many references including Orntoft *et al.*, Hyman *et al.*, and Pollack *et al.*

Collectively, Appellants submit that the Examiner's concerns in this rejection are misplaced and cannot properly form the basis for utility rejections of the present claims.

## **II. *Claim Rejections Under 35 U.S.C. §112, First Paragraph - Enablement***

Claims 39-43 stand rejected under 35 U.S.C. §112, first paragraph, for allegedly containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains or with which it is most nearly connected, to make and/or use the invention.

Appellants disagree for the reasons previously presented in Appellants Brief and in the discussion presented herein under Claim Rejections under 35 USC §101. Appellants submit that, as discussed above, the antibodies to the PRO269 polypeptide have utility in the diagnosis of lung cancers. Based on such a utility, one of skill in the art would know exactly how to use the claimed antibodies, for example, for diagnosis of cancer without any undue experimentation.

### CONCLUSION

For the reasons given above, Appellants submit that the present specification clearly describes, details and provides a patentable utility for the claimed invention. Moreover, it is respectfully submitted that based upon this disclosed patentable utility, the present specification clearly teaches "how to use" the presently claimed antibodies and provides an adequate written description of the claimed genus. As such, Appellants respectfully request reconsideration and reversal of the outstanding rejections of Claims 39-43.

The Commissioner is authorized to charge any fees which may be required, including extension fees, or credit any overpayment to Deposit Account No. 05-4634 (referencing Attorney's Docket No. 123851-181890 (GNE-1618 P2C34).

Respectfully submitted,

Date: January 2, 2009

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